



## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Payne, David  
Lonsdale, John  
Milner, Peter  
Pearson, Stewart
- (ii) TITLE OF INVENTION: FAB I
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Dechert Price & Rhoads  
(B) STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre  
(C) CITY: Philadelphia  
(D) STATE: PA  
(E) COUNTRY: US  
(F) ZIP: 19103
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: Windows 95  
(D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 60/024,845  
(B) FILING DATE: 28-AUG-1996
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Falk, Stephen T  
(B) REGISTRATION NUMBER: 36,795  
(C) REFERENCE/DOCKET NUMBER: GM50005
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 215-994-2488  
(B) TELEFAX: 215-994-2222  
(C) TELEX:

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GROUP 1800

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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ATGTTAAATC TTGAAAACAA AACATATGTC ATCATGGGAA TCGCTAATAA GCGTAGTATT
60
GCTTTTGGTG TCGCTAAAGT TTTAGATCAA TTAGGTGCTA AATTAGTATT TACTTACCGT 1
20
AAAGAACGTA GCCGTAAAGA GCTTGAAAAA TTATTAGAAC AATTAAATCA ACCAGAAGCG 1
80
CACTTATATC AAATTGATGT TCAAAGCGAT GAAGAGGTTA TTAATGGTTT TGAGCAAATT 2
40
GGTAAAGATG TTGGCAATAT TGATGGTGTA TATCATTCAA TCGCATTTGC TAATATGGAA 3
00
GACTTACGCG GACGCTTTTC TGAAACTTCA CGTGAAGGCT TCTTGTTAGC TCAAGACATT 3
60
AGTTCTTACT CATTACAAT TGTGGCTCAT GAAGCTAAAA AATTAATGCC AGAAGGTGGT 4
20
AGCATTGTTG CAACAACATA TTTAGGTGGC GAATTCGCAG TTCAAATTA TAATGTGATG 4
80
GGTGTGCTA AAGCGAGCTT AGAAGCAAAT GTTAAATATT TAGCATTAGA CTTAGGTCCT 5
40
GATAATATTC GCGTTAATGC AATTTCAGCT GGTCCAATCC GTACATTAAG TGCAAAAGGT 6
00
GTGGGTGGTT TCAATACAAT TCTTAAAGAA ATCGAAGAGC GTGCACCTTT AAAACGTAAC 6
60
GTTGATCAAG TAGAAGTAGG TAAAACAGCG GCTTACTTTR TAAGTGA CTT ATCAAGTGGC 7
20
GTTACAGGTG AAAATATTCA TGTAGATAGC GGATTCCACG CAATTAAATA A 7
71

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## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Asn Leu Glu Asn Lys Thr Tyr Val Ile Met Gly Ile Ala Asn

1		5		10		15									
Lys	Arg	Ser	Ile	Ala	Phe	Gly	Val	Ala	Lys	Val	Leu	Asp	Gln	Leu	Gly
		20						25					30		
Ala	Lys	Leu	Val	Phe	Thr	Tyr	Arg	Lys	Glu	Arg	Ser	Arg	Lys	Glu	Leu
		35					40					45			
Glu	Lys	Leu	Leu	Glu	Gln	Leu	Asn	Gln	Pro	Glu	Ala	His	Leu	Tyr	Gln
		50				55					60				
Ile	Asp	Val	Gln	Ser	Asp	Glu	Glu	Val	Ile	Asn	Gly	Phe	Glu	Gln	Ile
65					70					75				80	
Gly	Lys	Asp	Val	Gly	Asn	Ile	Asp	Gly	Val	Tyr	His	Ser	Ile	Ala	Phe
				85					90					95	
Ala	Asn	Met	Glu	Asp	Leu	Arg	Gly	Arg	Phe	Ser	Glu	Thr	Ser	Arg	Glu
			100					105					110		
Gly	Phe	Leu	Leu	Ala	Gln	Asp	Ile	Ser	Ser	Tyr	Ser	Leu	Thr	Ile	Val
		115					120					125			
Ala	His	Glu	Ala	Lys	Lys	Leu	Met	Pro	Glu	Gly	Gly	Ser	Ile	Val	Ala
	130					135					140				
Thr	Thr	Tyr	Leu	Gly	Gly	Glu	Phe	Ala	Val	Gln	Asn	Tyr	Asn	Val	Met
145					150					155				160	
Gly	Val	Ala	Lys	Ala	Ser	Leu	Glu	Ala	Asn	Val	Lys	Tyr	Leu	Ala	Leu
			165						170					175	
Asp	Leu	Gly	Pro	Asp	Asn	Ile	Arg	Val	Asn	Ala	Ile	Ser	Ala	Gly	Pro
			180					185					190		
Ile	Arg	Thr	Leu	Ser	Ala	Lys	Gly	Val	Gly	Gly	Phe	Asn	Thr	Ile	Leu
		195					200					205			
Lys	Glu	Ile	Glu	Glu	Arg	Ala	Pro	Leu	Lys	Arg	Asn	Val	Asp	Gln	Val
	210					215					220				
Glu	Val	Gly	Lys	Thr	Ala	Ala	Tyr	Leu	Leu	Ser	Asp	Leu	Ser	Ser	Gly
					230					235					240
225															
Val	Thr	Gly	Glu	Asn	Ile	His	Val	Asp	Ser	Gly	Phe	His	Ala	Ile	Lys
				245					250					255	